Phyre^2

Email	l.a.kelley@imperial.ac.uk
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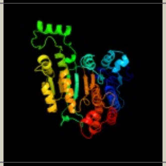
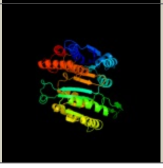
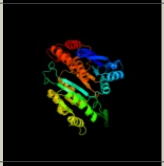
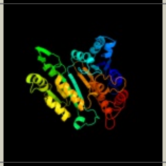
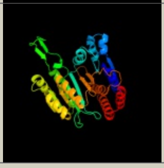
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pb1a_	Alignment		100.0	100	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
2	c2d4vD_	Alignment		100.0	66	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** crystal structure of nad dependent isocitrate dehydrogenase2 from acidithiobacillus thiooxidans
3	d1hqsa_	Alignment		100.0	69	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
4	c2e0cA_	Alignment		100.0	53	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**409aa long hypothetical nadp-dependent isocitrate **PDBTitle:** crystal structure of isocitrate dehydrogenase from sulfolobus tokodaii2 strain7 at 2.0 a resolution
5	c1tyoA_	Alignment		100.0	52	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** isocitrate dehydrogenase from the hyperthermophile aeropyrum pernix in2 complex with etheno-nadp
6	c2d1cB_	Alignment		100.0	40	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** crystal structure of tt0538 protein from thermus thermophilus hb8
7	d1cm7a_	Alignment		100.0	27	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
8	c3fmxX_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**tartrate dehydrogenase/decarboxylase; **PDBTitle:** crystal structure of tartrate dehydrogenase from pseudomonas2 putida complexed with nadh
9	d1v53a1	Alignment		100.0	27	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
10	d1vlca_	Alignment		100.0	31	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
11	d1cnza_	Alignment		100.0	27	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases

12	d1g2ua_	Alignment		100.0	29	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
13	c3r8wC_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**3-isopropylmalate dehydrogenase 2, chloroplastic; **PDBTitle:** structure of 3-isopropylmalate dehydrogenase isoform 2 from2 arabidopsis thaliana at 2.2 angstrom resolution
14	d1xaca_	Alignment		100.0	29	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
15	d1a05a_	Alignment		100.0	28	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
16	c2iv0A_	Alignment		100.0	57	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** thermal stability of isocitrate dehydrogenase from2 archaeoglobus fulgidus studied by crystal structure3 analysis and engineering of chimers
17	c3u1hA_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydrogenase; **PDBTitle:** crystal structure of ipmdh from the last common ancestor of bacillus
18	d1wpwa_	Alignment		100.0	30	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
19	c1x0lB_	Alignment		100.0	36	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**homoisocitrate dehydrogenase; **PDBTitle:** crystal structure of tetrameric homoisocitrate dehydrogenase from an2 extreme thermophile, thermus thermophilus
20	d1w0da_	Alignment		100.0	32	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
21	c3blxL_	Alignment	not modelled	100.0	35	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**isocitrate dehydrogenase [nad] subunit 2; **PDBTitle:** yeast isocitrate dehydrogenase (apo form)
22	c1zorB_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** isocitrate dehydrogenase from the hyperthermophile thermotoga maritima
23	c3blxM_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**isocitrate dehydrogenase [nad] subunit 1; **PDBTitle:** yeast isocitrate dehydrogenase (apo form)
24	c3us8A_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase [nadp]; **PDBTitle:** crystal structure of an isocitrate dehydrogenase from sinorhizobium2 meliloti 1021
25	c2uxqB_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase native; **PDBTitle:** isocitrate dehydrogenase from the psychrophilic bacterium2 desulfotalea psychrophila: biochemical properties and3 crystal structure analysis
26	d1lwda_	Alignment	not modelled	100.0	23	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
27	c2qfyE_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**isocitrate dehydrogenase [nadp]; **PDBTitle:** crystal structure of saccharomyces cerevesiae mitochondrial nadp(+)-2 dependent isocitrate dehydrogenase in complex with a-ketoglutarate
28	d1t0la_	Alignment	not modelled	100.0	19	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like

						Family: Dimeric isocitrate & isopropylmalate dehydrogenases
29	d1ptma_	Alignment	not modelled	98.5	16	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
30	d1r8ka_	Alignment	not modelled	97.1	24	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
31	d1itwa_	Alignment	not modelled	96.7	16	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Monomeric isocitrate dehydrogenase
32	c2hi1A_	Alignment	not modelled	96.5	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**4-hydroxythreonine-4-phosphate dehydrogenase 2; **PDBTitle:** the structure of a putative 4-hydroxythreonine-4-phosphate2 dehydrogenase from salmonella typhimurium.
33	c2b0tA_	Alignment	not modelled	96.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp isocitrate dehydrogenase; **PDBTitle:** structure of monomeric nadp isocitrate dehydrogenase
34	c1yxoB_	Alignment	not modelled	96.1	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxythreonine-4-phosphate dehydrogenase 1; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic protein pdxa2 pa0593
35	c2choA_	Alignment	not modelled	72.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucosaminidase; **PDBTitle:** bacteroides thetaiotaomicron hexosaminidase with o-2 glcnacase activity
36	d2fpoa1	Alignment	not modelled	72.3	8	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
37	c1p84E_	Alignment	not modelled	64.0	26	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
38	c2fyuE_	Alignment	not modelled	62.9	29	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit, **PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
39	d1riea_	Alignment	not modelled	57.0	29	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
40	d3cx5e1	Alignment	not modelled	46.9	26	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
41	d1oria_	Alignment	not modelled	46.2	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
42	c1orhA_	Alignment	not modelled	41.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arginine n-methyltransferase 1; **PDBTitle:** structure of the predominant protein arginine methyltransferase prmt1
43	d2r9ga1	Alignment	not modelled	38.3	19	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**MgsA/YrvN C-terminal domain-like
44	c3pvsA_	Alignment	not modelled	37.5	13	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
45	c2nvgA_	Alignment	not modelled	35.6	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit; **PDBTitle:** soluble domain of rieske iron sulfur protein.
46	d2esra1	Alignment	not modelled	33.7	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
47	d2fhpa1	Alignment	not modelled	32.0	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
48	c3b3jA_	Alignment	not modelled	31.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-arginine methyltransferase carm1; **PDBTitle:** the 2.55 a crystal structure of the apo catalytic domain of2 coactivator-associated arginine methyl transferase i(carm1:28-507,3 residues 28-146 and 479-507 not ordered)
49	c1zn1L_	Alignment	not modelled	31.7	44	**PDB header:**biosynthetic/structural protein/rna **Chain:** L: **PDB Molecule:**30s ribosomal protein s12; **PDBTitle:** coordinates of rrf fitted into cryo-em map of the 70s post-2 termination complex
50	c2fynO_	Alignment	not modelled	31.0	32	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
51	d2fyta1	Alignment	not modelled	30.7	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
52	d2fcaa1	Alignment	not modelled	30.6	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like

53	d2uubl1	Alignment	not modelled	30.0	44	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
54	c2pebB_	Alignment	not modelled	29.2	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative dioxygenase; **PDBTitle:** crystal structure of a putative dioxygenase (npun_f1925) from nostoc2 punctiforme pcc 73102 at 1.46 a resolution
55	c3fzgA_	Alignment	not modelled	27.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methylase; **PDBTitle:** structure of the 16s rrna methylase arma
56	c3cesB_	Alignment	not modelled	27.3	30	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl modification enzyme **PDBTitle:** crystal structure of e.coli mnmg (gida), a highly-conserved trna2 modifying enzyme
57	d3bgea1	Alignment	not modelled	26.1	13	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**MgsA/YrvN C-terminal domain-like
58	d1f3la_	Alignment	not modelled	25.1	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
59	d1g6q1_	Alignment	not modelled	23.4	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
60	d1yzha1	Alignment	not modelled	23.4	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
61	c2e76D_	Alignment	not modelled	23.1	21	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
62	d2qall1	Alignment	not modelled	22.1	44	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
63	c3c6kC_	Alignment	not modelled	21.9	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**spermine synthase; **PDBTitle:** crystal structure of human spermine synthase in complex2 with spermidine and 5-methylthioadenosine
64	c1yy3A_	Alignment	not modelled	21.4	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:trna ribosyltransferase- **PDBTitle:** structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
65	d3ctda1	Alignment	not modelled	20.5	16	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**MgsA/YrvN C-terminal domain-like
66	c3p9nA_	Alignment	not modelled	19.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible methyltransferase (methylase); **PDBTitle:** rv2966c of m. tuberculosis is a rsmd-like methyltransferase
67	c3ku1E_	Alignment	not modelled	18.7	13	**PDB header:**transferase **Chain:** E: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of streptococcus pneumoniae sp1610, a2 putative trna (m1a22) methyltransferase, in complex with s-3 adenosyl-l-methionine
68	d1i94l_	Alignment	not modelled	18.3	44	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
69	c3pubA_	Alignment	not modelled	17.6	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**30kda protein; **PDBTitle:** crystal structure of the bombyx mori low molecular weight lipoprotein2 7 (bmlp7)
70	c2zkql_	Alignment	not modelled	17.0	39	**PDB header:**ribosomal protein/rna **Chain:** L: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
71	c1s1hL_	Alignment	not modelled	16.5	39	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**40s ribosomal protein s23; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
72	d1cyxa_	Alignment	not modelled	16.2	15	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
73	c1cyxA_	Alignment	not modelled	16.2	15	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cyoa; **PDBTitle:** quinol oxidase (periplasmic fragment of subunit ii with2 engineered cu-a binding site)(cyoa)
74	c3ctdB_	Alignment	not modelled	15.7	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative atpase, aaa family; **PDBTitle:** crystal structure of a putative aaa family atpase from2 prochlorococcus marinus subsp. pastoris
75	c3evzA_	Alignment	not modelled	15.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal strucure of methyltransferase from pyrococcus furiosus
76	d1uira_	Alignment	not modelled	15.1	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Spermidine synthase
						PDB header:transferase **Chain:** B: **PDB Molecule:**histone-arginine methyltransferase

77	c2v7eB_	Alignment	not modelled	14.9	14	carm1; **PDBTitle:** crystal structure of coactivator-associated arginine2 methyltransferase 1 (carm1), unliganded
78	d2p8ia1	Alignment	not modelled	14.6	14	**Fold:**Ferredoxin-like **Superfamily:**DOPA-like **Family:**DOPA dioxygenase-like
79	d1fftb1	Alignment	not modelled	14.3	15	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
80	c3g05B_	Alignment	not modelled	14.3	30	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl modification enzyme **PDBTitle:** crystal structure of n-terminal domain (2-550) of e.coli mnmg
81	c2xzmL_	Alignment	not modelled	14.2	33	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**40s ribosomal protein s12; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
82	d1i7na1	Alignment	not modelled	13.5	16	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Synapsin domain
83	d1u35c1	Alignment	not modelled	13.2	23	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
84	c2esrB_	Alignment	not modelled	12.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** conserved hypothetical protein- streptococcus pyogenes
85	d1inla_	Alignment	not modelled	12.0	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Spermidine synthase
86	c3e1tA_	Alignment	not modelled	12.0	21	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**halogenase; **PDBTitle:** structure and action of the myxobacterial chondrochloren2 halogenase cndh, a new variant of fad-dependent halogenases
87	d1f66c_	Alignment	not modelled	11.7	14	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
88	c1f66C_	Alignment	not modelled	11.7	14	**PDB header:**structural protein/dna **Chain:** C: **PDB Molecule:**histone h2a.z; **PDBTitle:** 2.6 a crystal structure of a nucleosome core particle2 containing the variant histone h2a.z
89	c3o2qB_	Alignment	not modelled	11.5	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
90	c2przB_	Alignment	not modelled	11.4	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase 1; **PDBTitle:** s. cerevisiae orotate phosphoribosyltransferase complexed2 with omp
91	d1kx3c_	Alignment	not modelled	11.4	16	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
92	c3bwbA_	Alignment	not modelled	11.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**spermidine synthase; **PDBTitle:** crystal structure of the apo form of spermidine synthase from2 trypanosoma cruzi at 2.5 a resolution
93	d1hioa_	Alignment	not modelled	10.9	16	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
94	d2o07a1	Alignment	not modelled	10.9	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Spermidine synthase
95	c2pssC_	Alignment	not modelled	10.9	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**spermidine synthase; **PDBTitle:** the structure of plasmodium falciparum spermidine synthase in its apo-2 form
96	d1n1jb_	Alignment	not modelled	10.8	11	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
97	c3o2sB_	Alignment	not modelled	10.5	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72 complex
98	d2jssa1	Alignment	not modelled	10.4	15	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
99	c3qd7X_	Alignment	not modelled	10.2	19	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized protein ydal; **PDBTitle:** crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli